

FIG. 1

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LINKER #1 15bp | SV40 ORIGIN=332bp
GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
GGAGAATGGG CGGAAC TGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
ATGTTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTGCTGG GAGGCGTGGG 240
GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCTGCT 300
GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAAT TAATTCCCCT 360
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTTCATA GCCCATATAT GGAGTTCCTG 420
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTTG 480
ACGTCATAAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC CCTGGCATTG TGCCCGATAC 660
ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
CATCACAGAT CTCTCACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG 1020
CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAATCA AAGGTACGGT GGCTGCACCA 1080
TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1140
TGCTGCTGA ATAACCTCTA TCCAGAGAGG GCCAAAGTAC AGTGAAGGT GGATAACGCC 1200
HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON
CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
AGCCTCAGCA GCACCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTACAA AGAGCTTCAA CAGGGGAGAG 1380
STOP
LIGHT CHAIN | Eco RI LINKER #4=85bp
TGTTCAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1440
GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500

FIG. 2A

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GTTTGCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCAC TGTCTTTCC 1560
 TAATAAAATG AGGAAATTGC **BGH poly A=231bp** ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
 GGGGTGGGCG AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680
 GCGGTGGGCT CTATGGAACC **LINKER #5=15bp** ACCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740
 1702'3 1717'8
 ACGTCAATGA CGGTAAATGG CCCGCCTGCG ATTATGCCCA GTACATGACC TTATGGGACT 1800
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGGTTT 1860
 GGCAGTACAT CAATGGGCGT **CMV PROMOTER-ENHANCER=334bp** GGATAGCGGT TTGACTCACG GGGATTTCOA AGTCTCCACC 1920
 CCATTGACGT CAATGGGAGT TTGTTTGGCG ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980
 GTAACAACCT CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
 TAAGCAGAGC **LINKER #6=7bp** TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2100
 2051'2 2058'9 **Sal I**
 ATCGGTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG **LEADER=51bp** CTACCGGTGT **Mlu I 2151'2 Nhe I** CGCTAGCACC 2160
 START HEAVY CHAIN -5 -4 -3 114 115
 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220
 GCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGC GTGGAACCTCA 2280
 GGGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC 2340
 TCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
HUMAN GAMMA 1 CONSTANT
 AACGTGAATC ACAAGCCCAAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
 GACAAAACCT ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
 TTCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGACCCC TGAGGTCA 2580
 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
 CGTGTGGTCA GCGTCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGACTACAAG 2760
 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAGG 2880
 AACCAGGTCA GCCTGACCTG CCTGGTCAA GGCCTCTATC CCAGCGACAT CGCCGTGGAG 2940
 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

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GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
STOP HEAVY CHAIN | Bam HI **LINKER #7=81bp**
CTCTCCCTGT CTCGGGTAA **ATGAGGATCC** GTTAACGGTT ACCAAGTACC TAGACTGGAT 3180
3144 5
TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC **CTCGACTGTG** CCTTCTAGTT 3240
3225 6
GCCAGCCATC TGTGTTTTCG CCTTCCCCCG TGCCTTCCTT GACCTTGAA GGTGCCACTC 3300
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
CCACTGTCTT TTCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360
CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA 3420
LINKER #8=34bp
GGCATGCTGG GGATGCGGTG GGCTCTATGG **AACCACTGG** GGCTCGACAG CGCTGGATCT 3480
3456 7
CCCGATCCCC **AGCTTTGCTT** CTCAATTCTT TATTTCATA ATGAGAAAAA AAGGAAAAAT 3540
3490 1
AATTTTAACA CCAATTACAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
MOUSE BETA GLOBIN MAJOR PROMOTER=368bp
AGACAGTGT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
GACTCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780
GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 3840
LINKER #9=19bp **5' UNTRANSLATED DHFR=82bp**
CTGACATAGT TGTGTGGGA GCTTGGATAG **CTTGACAGC** TCAGGGCTGC GATTTCGCGC 3900
3856 7 3875 6
START DHFR
CAAACCTGAC GGCAATCTTA GCGTGAAGGC TGGTAGGATT TTATCCCCGC **TGCCATCAT** 3960
3957 8
GTTCGACCAT TGAAGTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG CAAGAACGGA 4020
GACCTACCTT GGCCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080
TCTTCAGTGG AAGGTAACA GAATCTGGTG ATTATGGGTA GGAACACCTG GTTCTCCATT 4140
MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON
CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAA 4200
GAACCAACCAC GAGGAGCTCA TTTTCTTGCC AAAAGTTTGG ATGATGCCTT AAGACTTATT 4260
GAACAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTTGGA TAGTCGGAGG CAGTTCTGTT 4320
TACCAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
GAATTTGAAA GTGACACGTT TTTCCAGAA ATTGATTTGG GGAATATATA ACTTCTCCCA 4440
GAATACCCAG GCGTCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTTGAA 4500

FIG. 2C

GTCTACGAGA AGAAAGACTA **STOP DHFR** 4521'2 CAGGAAGAT GCTTCAAGT TCTCTGCTCC C~~CT~~CCTAAAG 4560
 3' UNTRANSLATED DHFR=82bp **LINKER #10=10bp**
 TCATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGGC 4620
 4603'4 4613'4
 TTCTAGTTGC CAGCCATCTG TTGTTTGCCC CTCCCCCGTG CTTCTCTTGA CCCTGGAAGG 4680
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 TGCCACTCCC ACTGTCCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740
 GTGTCAATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA **LINKER #11=17bp**
 CCAGCTGGGG CTCGAGCTAC 4844'5 4850
 TAGCTTTGCT TCTCAATTC TTATTTGCAT AATGAGAAAA AAAGAAAAA TAATTTTAAC 4920
 ACCAATTCAG TAGTTGATTG AGCAAAATGCG TTGCCAAAAA GGATGCTTTA GAGACAGTGT 4980
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCGACAGCTG AGACTCCTA 5040
 GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATACCGGA AGCCTGATTG 5100
 CGTAGAGCCA CACCTTGGA AGGGCCAATC TGCTACACA GGATAGAGAG GGCAGGAGCC 5160
 AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTTGCT TCTGACATAG 5220
LINKER #12=21bp **START NEO**
 TTGTGTTGGG AGCTTGGATC GATCCTCTAT GGTGGAACAA GATGGATTGC ACGCAGGTTG 5280
 5227'8 5248'9
 TCCGGCCGCT TGGGTGGAGA GGCTATTCGG CTATGACTGG GCACAACAGA CAATCGGCTG 5340
 CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGGCG CCGGTTCTTT TTGTCAAGAC 5400
 NEOMYCIN PHOSPHOTRANSFERASE
 CGACCTGTCC GGTGCCCTGA ATGAACTGCA GGACGAGGCA GCGGGCTAT CGTGCGTGGC 5460
 795bp=264 AMINO ACIDS & STOP CODON
 CACGACGGGC GTTCCTTGGC CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520
 GCTGTATTG GCGGAAGTGC CGGGGCAGGA TCTCTGTCA TCTACCTTG CTCTGCGCG 5580
 GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640
 CCCATTGCAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGAAGCCGG 5700
 TCTTGTGCAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760
 CGCCAGGCTC AAGGCGCGCA TGCCCGACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820
 CTGCTTGGCG AATATCATGG TGGAAAAATG CCGCTTTTCT GGATTCATCG ACTGTGGCCG 5880
 GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940
 GCTTGGCGGC GAATGGGCTG ACCGCTTCTT CGTGCTTTAC GGTATCGCG CTGCCGATTC 6000

FIG. 2D

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CGACGCGATC GCCTTCTATC GCCTTCTTGA STOP NEO1
CGAGTCTTTC TCGACGGGAC TCTGGGGTTC 6060
604314

GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCAGGAG ATTTTCGATTC CACCGCGCGC 6120

TTCTATGAAA GGTGGGGCTT 3' UNTRANSLATED NEO=173bp
CGGAATCGTT TTCCGGGACG CCGGCTGGAT GATCTCCAG 6180

CGCGGGGATC TCATGCTGGA GTTCTTCGCC CACCCCAACT TGTATTATGC AGCTTATAAT 6240
621617

GGTACAAAT AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TTCACTGCAT 6300

TCTAGTTGTG GTTTGTCCAA SV40 POLY A EARLY=133bp LINKER #13=19bp
ACTCATCAAT CTATCTTATC ATGCTCTGGAT CGCGGCCGCG 6360
6349150

ATCCCGTCTGA GAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC 6420
636819

CGCTCACAAAT TCCACACAAC ATACGAGCGG GAAGCATAAA GTGTAAAGCC TGGGGTGCC 6480

AATGAGTGAG CTAACCTACA TTAATTGCGT TGCCTCACT GCCCGCTTTC CAGTCGGGAA 6540

ACCTGTCGTG CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTCGCGTA 6600

TTGGGCGCTC TTCCGCTTCC TCGCTCACTG PVC 19
ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC 6660

GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAAATCA GGGGATAACG 6720

CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT 6780

TGCTGGCGTT TTTCCATAGG 6792=BACTERIAL ORIGIN OF REPLICATION
CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA 6840

GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATACCA GCGCTTTCCC CCTGGAAGCT 6900

CCCTCGTGCG CTCTCTGTT CCGACCCCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC 6960

CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020

TCGTTGCTC CAAGCTGGGC TGTGTGCACG AACCCCCCGT TCAGCCCGAC CGCTGCGCCT 7080

TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG 7140

CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA 7200

AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA 7260

AGCCAGTTAC CTTCCGAAAA AGAGTTGGTA GCTCTTGATC CGGCAAAACA ACCACCGCTG 7320

GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC AGATTACGCG CAGAAAAAAA GGATCTCAAG 7380

AAGATCCTTT GATCTTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAA TCACGTTAAG 7440

GGATTTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAAAAAT 7500

FIG. 2E

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GAAGTTTAA ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT 7560
 TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTTCG TTCATCCATA GTTGCCCTGAC 7520
 TCCCGCTCGT GTAGATAACT ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680
 TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTATC AGCAATAAAC CAGCCAGCCG 7740
 GAAGGGCCGA GCGCAGAAGT GGTCTTGCAA CTTTATCCGL CTCCATCCAG TCTATTAATT 7800
 GTTGCCGGGA AGCTAGAGTA AGTAGTTCCG CAGTTAATAG TTTGCGCAAC GTTGTGGCA 7860
 TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC AGCTCCGGTT 7920
 CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAGCG GTTAGCTCCT 7980
 TCGGTCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCACT GTTATCACTC ATGGTTATGG 8040
 CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG 8100
 AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG 8160
 CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220
 AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCGATGT 8280
 AACCCTCTCG TGCACCAAC TGATCTTCAG CATCTTTTAC TTTCAACAGC GTTTCTGGGT 8340
 GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGCGGACA CGGAAATGTT 8400
 GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
 TGAGCGGATA CATATTTGAA TGTATTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT 8520
 TTCCCCGAAA AGTGCCACCT

FIG. 2F

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LINKER #1=15bp
GACGTCCGG CCGCTCTAGG CCTCCAAAA AGCCTCTCA CTACTTCTGG AATAGCTCAG 60
15'6

AGGCCGAGGC GGCTCCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120

GGAGAATGGG CGGAAC TGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180
SV40 ORIGIN=332bp

ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTGCTGG GGAGCCTGGG 240

GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300

GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAAT TAATCCCTCT 360
LINKER #2=13bp
347'8

AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCGGC 420

GTTACATAAC TTACGGTAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480

ACGTCATAAA TGACGATATG TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540

TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
CVM PROMOTER-ENHANCER=567bp

AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TCCCAAGTAC 660

ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720

ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT ACGGTTTGA CTCACGGGGA 780

TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGC 840

GACTTTCCAA AATGTCGTAA CAATCCGCC CCATTGACGC AAATGGCGCG TAGGCGTGTA 900

CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTTGAACC GTCAGATCGC CTGGAGAGCG 960
LINKER #3=7bp
927'8 934'5

Bgl 2 | START LIGHT CHAIN NATURAL LEADER=66bp
CATCACAGAT CTCTCACTAT GCATTTTCAG GTGCAGATTA TCAGTTCTCT GCTAATCAGT 1020
978'9

GCTTCAGTCA TAATGTCCAG AGGACAAAT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
1044'5+1

GCATCTCCAG GGGAGAAAGT CACAATGACT TGCAGGGCCA GCTGAAGTGT AAGTTACATC 1140

CACTGGTTCC AGCAGAAGCC AGGATCTCC CCCAAACCCCT GGATTTATGC CACATCCAAC 1200

CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTA CTCTCTC 1260
LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID

ACCATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320

AACCCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGTT GGCTGCACCA 1380
1362'3

TCTGTCTTCA TCTTCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCTGTTGTG 1440

TGCTGTCTGA ATAAC TTCTA TCCAGAGAG GCCAAAGTAC AGTGAAGGT GGATAACGCC 1500

FIG. 3A

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HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
 AGCCTCAGCA GCACCTTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
 TGGCAAGTCA CCCATCAGGG CCGTAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680
 STOP
 LIGHT
 CHAIN Eco RI LINKER #4=81bp
 TGTTCGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACAATGC 1740
 1646 17
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
 1771 12
 GTTTGCCCT CCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCAC TGTCTTTCC 1860
 TAATAAAATG AGGAAATTGC ATCGATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGTG 1920
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 GGGGTGGGGC AGGACAGCAA GGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
 GCGGTGGGCT CTATGGAACC ACTGGGGCT CGACAGCTAT GCCAAGTACG CCCCTATTG 2040
 2002 13 2017 8
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160
 CMV PROMOTER-ENHANCER=334bp
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCAGG GGGATTCCCA AGTCTCCACC 2220
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAATCA ACGGGACTTT CCAAATGTC 2280
 GTAACAACCT CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2340
 LINKER #6=7bp Sal I
 TAAGCAGAGC TGGGTACCTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400
 2351 2 2358 9
 START
 HEAVY CHAIN SYNTHETIC & NATURAL LEADER Mlu I 2457 8
 ATGGGTTGGA GCCTCATCTT GCTCTTCTT GTCGCTGTTG CTACGGGTGT CCGTCTCCAG 2460
 2401 -5 -4 -3 -2 -1 +1
 GTACAACCTGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTCC 2520
 TGCAAGGCTT CTGGCTACAC ATTTACCACT TACAATATGC ACTGGGTAAAC ACAGACACCT 2580
 HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID
 GGTGGGGGCC TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640
 CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
 TACGGCGGTG ACTGCTACTT CAATGTCTGG GCGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
 Nhe I
 GCTAGCACCA AGGGCCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 2880
 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGT GACGGTGTCTG 2940
 HUMAN GAMMA 1 CONSTANT=993bp
 TGGAACTCAG GCGCCCTGAC CAGCGCGGTG CACACCTTCC CGGCTGTCTT ACAGTCTCA 3000

FIG. 3B

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330 AMINO ACID & STOP CODON
GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3060
TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
AAATCTTGTG ACAAACACTA CACATGCCCA CCGTGCCCGAG CACCTGAACT CCTGGGGGGA 3180
CCGTCACTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCTT 3240
GAGGTCACAT CGCTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
TACGTGGACG CGCTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
GAGTACAAGT GCAAGGTCTC CAACAAGGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480
AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCATC CCGGGATGAG 3540
CTGACCAAGA ACCAGGTGAG CCGTACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600
GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAAC AACAAGACCAC GCCTCCCGTG 3660
CTGGACTCCG ACGGCTCCTT CTTCCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720
CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA ITGAGGATCCG LINKER #7=81bp
3813'4 TTAACGGTTA CCAACTACCT 3840
AGACTGGATT CGTGACAACA TGCGGCCGTG ATATCTACGT ATGATCAGCC TCGACTGTGC 3900
3894'5
CTTCTAGTTG CCAGCCATCT GTTGTTTGCC CCTCCCCCGT GCCTTCTCTG ACCCTGGAAE 3960
GTGCCACTCC CACTGTCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGCTGAGTA 4020
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
GGTGTCACTC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGGAG GATTGGGAAG 4080
ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140
4125'6
GCTGGATCTC CCGATCCCCA GCTTTGCTTC TCAATTTCTT ATTTGCATAA TGAGAAAAAA 4200
AGGAAAAATTA ATTTTAACAC CAATTCACTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
ATGCTTTAGA GACAGTGGTC TCTGCACAGA TAAGGACAAA CATTATTCTG AGGGAGTACC 4320
CAGAGCTGAG ACTCCTAAGC CAGTGAGTGG CACAGCATTC TAGGGAGAAA TATGCTTGTC 4380
ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGTAAG GGCCAATCTG CTCACACAGG 4440
ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500

FIG. 3C

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LINKER #9=19bp [5' UNTRANSLATED DHFR=82bp
 CATTTCCTTC TGACATAGTT GTCTGGGAG CTTGGATAGC TTGCACAGCT CAGGGCTGCG 4560
 4525 16 4544 5

ATTTCGCGCC AAACCTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATT TATCCCCGCT 4620

START DHFR
 GCCATCTGGC TTCCAGCATT GAACTGCATC GTCGCCGTGT CCAAAAATAT GGGGATTGGC 4680
 4626 7

AAGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740

ACCAACAACCT CTTCAGTGGA AGGTAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800

DHFR=564bp=187 AMINO ACID & STOP CODON
 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860

GAACCTAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGA TGATGCCTTA 4920

AGACTTATTG AACAAACCGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980

AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040

ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCCAGAAA TTGATTTGGG GAAATATAAA 5100

CTTCTCCCAG AATACCCAGG CGTCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160

STOP DHFR 3' UNTRANSLATED DHFR=82bp
 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGT CTCTGCTCCC 5220
 5140 1

CTCCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA GATCAGCCTC 5280
 =10bp, 5272 3

GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGGCCC TCCCCGTGC CTTCCTTGAC 5340

BOVINE GROWTH HORMONE POLYADENYLATION=231bp
 CCTGGAAGGT GCCACTCCCA CTGTCCTTTC CTAATAAAAT GAGGAATTTG CATCGCATTG 5400

TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460

TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TCGGTGGGGC TCTATGGAAC CAGCTGGGGC 5520
 =17bp, 5513 4

TCGAGCTACT AGCTTTGCTT CTCAAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAAAT 5580
 5530 1

AATTTTAACA CCAATTCACT AGTTGATTGA GCAATGCGT TGCCAAAAAG GATGCTTTAG 5640

MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA CTAGGGAGAA ATATGCTTGT CATCACCAGG 5700

GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCAGG 5760

GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820

GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCTC ACATTTGCTT 5880

LINKER #12=21bp [START NEO
 CTGACATAGT TGTGTTGGA GCTTGGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
 5896 7 5917 8

CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTGGGC TATGACTGGG CACAACAGAC 6000

FIG. 3D

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AATCGGCTGC TCTGATGCCG CCGTGTTCGG GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT 6060
NEOMYCIN PHOSPHOTRANSFERASE=795bp=264 AMINO ACID & STOP CODON
 TGTCGAAGACC GACCTGTCCG GTGCCCTGAA TGAAGTCAGS GACGAGGCAG CGCGGCTATC 6120
 GTGGCTGGCC ACGACGGGCG TTCCTTGGCG AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
 AAGGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCTGTCTAT CTCACCTTGC 6240
 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCCG CGGCTGCATA CGCTTGATCC 6300
 GGCTACCTGC CCATTGACCC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
 GGAAGCCGGT CTTGTGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
 CGAACTGTTT GCCAGGCTCA AGCGCGCAT GCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
 TGGCGATGCC TGCTTGGCGA ATATCATGGT GAAAAATGGC CGCTTTTCTG GATTATCGA 6540
 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGCACATA CGCTTGGCTA CCCGTGATAT 6600
 TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCTCT GTGCTTTATG GTATCGGCGC 6660
 TCCCGATTCT CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTCTCTCT **STOP NEOI**
 6712'3
 CTGGGGTTCT AAATGACCGA CCAAGCGAGC CCCAACCTGC CATCAGGAGA TTTGATTC 6780
 ACCGCCGCCT TCTATGAAAG **3' UNTRANSLATED NEO=173bp**
 GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840
 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTGGCTC **ACCCCAACTT**
 6885'6
 GCTTATAATG GTTACAATA AAGCAATAGC ATCACAATT TCACAAATA AGCATTTTTT 6960
 TCATGCAATT CTAGTTGTGG TTGTGCCAAA CTCATCAATC TATCTTATCA TGCTGGATC 7020
SV40 EARLY POLYADENYLATION REGION=133bp
LINKER #13=19bp
 GCGGCCGCGA **TCCCGTCTAG**
 7037'8
 AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
PUC 19
 ATTGTTATCC GCTCACAAAT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAGCCT 7140
 GGGGTGCTTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTTC 7200
 AGTCGGGAAA CCTGTGCTGC CAGCTGCATT AATGAATCG CCAACGCCGC GGGAGAGGCG 7260
 GTTTGCGTAT TGGGCGCTCT TCGCTTCTCT CGCTCACTGA CTCGCTGCGC TCGGTGTTTC 7320
 GGCTCGGCGC AGCGGTATCA GCTACTCAA AGCGCGTAAT ACGGTTATCC ACAGAATCAG 7380
 GGGATAACGC AGGAAGAAGC ATGTGAGCAA AAGGCCAGCA AAAGCCCAAG AACCGTAAAA 7440
7461=BACTERIAL ORIGIN OF REPLICATION
 AGGCCGCGTT GCTGGCGTTT **TTCATAGGC** TCCGCCCCCC TGACAGCAT CACAAAAATC 7500

FIG. 3E

GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC 7560
 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTGCGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC 7740
 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTCGGAAGAA GAGTTGGTAG CTCTTGATCC GGCAACAAC 7980
 CCACCGCTGG TAGCGGTGGT TTTTTTGTTC GCAAGCAGCA GATTACGGCG AGAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT 8100
 CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAGGAT CTTACCTAG ATCCTTTTAA 8160
 ATTAATAATG AAGTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT ^{STOP} 8220
BETA LACTAMASE
 ACCAATGCTT AATCAGTAGG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG 8280
 TTGCCTGACT CCCCGCTGTG TAGATACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAAC 8400
 BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON
 AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTGCCC AGTTAATAGT TTGCGCAACG 8520
 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA 8580
 GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8540
 TTAGTCTCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA 8700
 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTGATGCC ATCCGTAAGA TGCTTTTCTG 8760
 TGA CTGCTGTA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGCGCA CCGAGTTGCT 8820
 CTGCGCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
 TCATTGGAAC ACGTTCTTCG GGGCGAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
 GGTGATGTA ACCCACTCGT GCACCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG 9000
 TTTCTGGGTG AGCAAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGCGCACAC 9060
 GGAAATGTTG AATACCTATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 ATGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTT 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT

FIG. 3F

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LEADER

FRAME 1 Met Asp -20 Gln Val Gln Ile -15 Ser Phe Leu Leu -10 Ser Ala Ser Val
 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC
 987 996 1005 1014 1023

-5 Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser
 ATA ATG TCC AGA GGA CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT
 1038 1047 1056 1065 1074 1083

Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His
 CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AGT TAC ATC CAC
 1095 1104 1113 1122 1131 1140

35 FR2 40 45 49 50 CDR2
 Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn
 TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC
 1152 1161 1170 1179 1188 1197

55 56 57 60 FR3 65 70
 Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
 CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC AGC GGG TCT GGG ACT TCT TAC TCT
 1209 1218 1227 1236 1245 1254

75 80 85 88 89 90
 Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 CTC ACC ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG
 1266 1275 1284 1293 1302 1311

CDR3 95 97 98 100 FR4 105 107
 Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA
 1323 1332 1341 1350 1359

FIG. 4

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LEADER

-19	-15	-10	-5
FRAME 1 Met Gly Trp Ser	Leu Ile Leu Leu Phe	Leu Val Ala Val Ala Thr Arg Val	
ATG GGT TGG AGC	ATC TTG CTC TTC	CTT GTC GGT GTT GCT ACG GGT	CTC
2409	2418	2427	2436 2445
-1	+1	FR1	10
Leu Ser	Gln Val Gln Leu	Gln Gln Pro Gly Ala	Glu Leu Val Lys Ala Gly Ala Ser
CTG TCC	CAG GTA CAA CTG	CAG CAG CCT GGG GCT	GAG CTG AAG CCT GGG GCC TCA
2460	2469	2478	2487 2496 2505
20	25	30	31 CDR1 35 36
Val Lys Met Ser Cys Lys	Ala Ser Gly Tyr Thr Phe Thr	Ser Tyr Asn Met His Trp	
GTG AAG ATG TCC TGC AAG	GCT TCT GGC TAC ACA TTT ACC	AGT TAC AAT ATG CAC TGG	
2517	2526	2536	2544 2553 2562
40	FR2	45	49 50 52 52A 53 54
Val Lys Gln Thr Pro Gly	Arg Gly Leu Glu Trp Ile Gly	Ala Ile Tyr Pro Gly Asn	
GTA AAA CAG ACA CCT GGT	CGG GGC CTG GAA TGG ATT GGA	GCT ATT TAT CCC CGA AAT	
2574	2583	2592	2601 2610 2619
55	CDR2	60	65 66 FR3 70
Gly Asp Thr Ser Tyr Asn	Gln Lys Phe Lys Gly	Lys Ala Thr Leu Thr Ala Asp Lys	
GGT GAT ACT TCC TAC AAT	CAG AAG TTC AAA GGC	AAG GCC ACA TTG ACT GCA GAC AAA	
2631	2640	2649	2658 2667 2676
75	80	82 82A 82B 82C 83	85
Ser Ser Ser Thr Ala Tyr	Met Gln Leu Ser Ser Leu Thr	Ser Gln Asp Ser Ala Val	
TCC TCC AGC ACA GCC TAC	ATG CAG CTC AGC AGC CTG ACA	TCT GAG GAC TCT GCG GTC	
2688	2697	2706	2715 2724 2733
90	94 95	CDR3	100 100A 100B 100C 100D 101 102 103
Tyr Tyr Cys Ala Arg	Ser Thr Tyr Tyr Gly Gly	Asp Trp Tyr Phe Asn Val	Trp Gly
TAT TAC TGT GCA AGA	TCG ACT TAC TAC GGC	GGT GAC TGG TAC TTC AAT	GTC TGG GGC
2745	2754	2763	2772 2781 2790
105 FR4	110	113	
Ala Gly Thr Thr Val Thr	Val Ser Ala		
GCA GGG ACC ACG GTC ACC	GTC TCT GCA		
2802	2811	2820	

FIG. 5

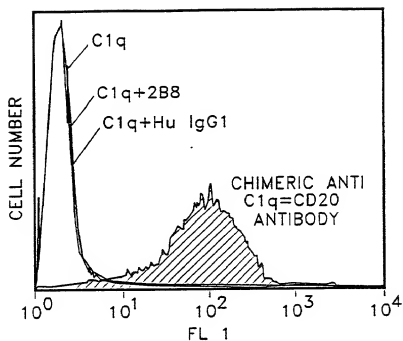


FIG. 6

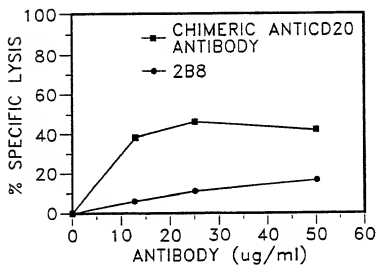


FIG. 7

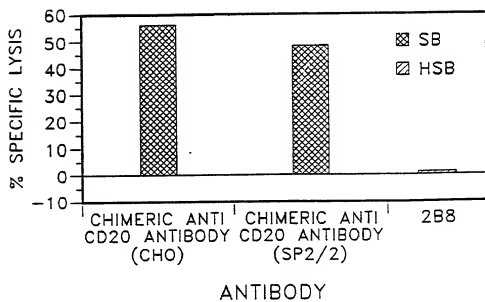


FIG. 8

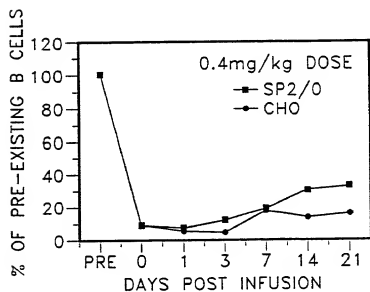


FIG. 9A

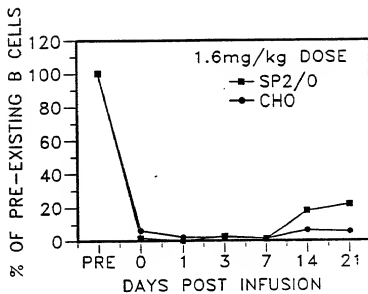


FIG. 9B

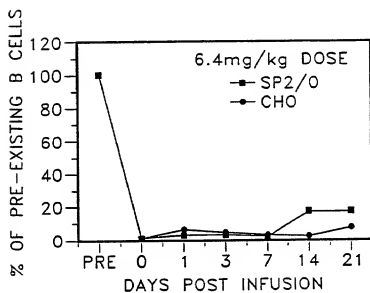


FIG. 9C

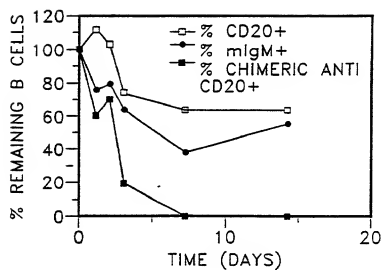


FIG. 10

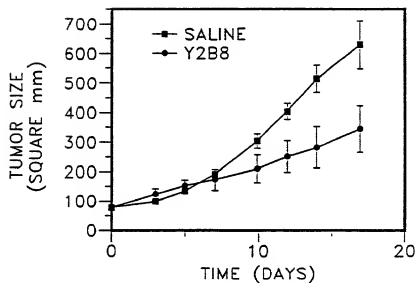


FIG. 11

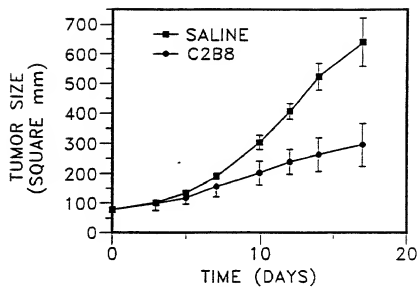


FIG. 12

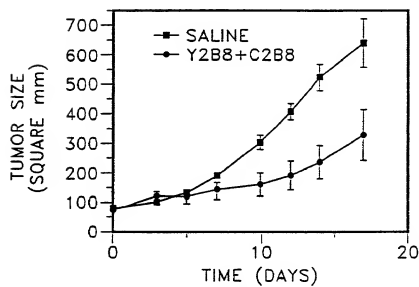


FIG. 13

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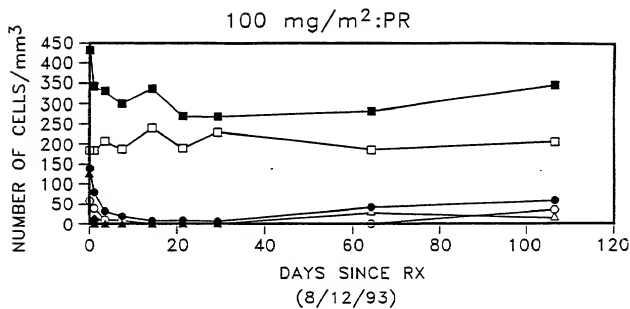


FIG. 14A

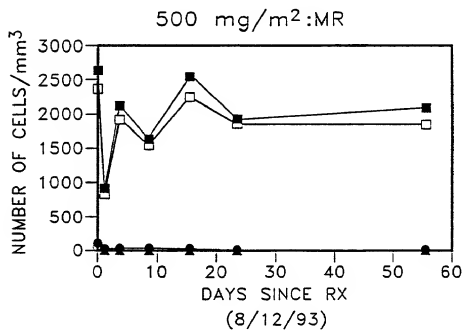


FIG. 14B